

# Package ‘seqcombo’

January 4, 2025

**Title** Visualization Tool for Genetic Reassortment  
**Version** 1.29.0  
**Description** Provides useful functions for visualizing virus reassortment events.  
**Depends** R (>= 3.4.0)  
**Imports** ggplot2, grid, igraph, utils, yulab.utils  
**Suggests** emojiFont, knitr, rmarkdown, prettydoc, tibble  
**VignetteBuilder** knitr  
**ByteCompile** true  
**License** Artistic-2.0  
**Encoding** UTF-8  
**BugReports** <https://github.com/GuangchuangYu/seqcombo/issues>  
**biocViews** Alignment, Software, Visualization  
**RoxygenNote** 7.3.0  
**git\_url** <https://git.bioconductor.org/packages/seqcombo>  
**git\_branch** devel  
**git\_last\_commit** 10d9bfc  
**git\_last\_commit\_date** 2024-10-29  
**Repository** Bioconductor 3.21  
**Date/Publication** 2025-01-03  
**Author** Guangchuang Yu [aut, cre]  
**Maintainer** Guangchuang Yu <guangchuangyu@gmail.com>

## Contents

seqcombo-package . . . . .	2
geom_genotype . . . . .	2
geom_hybrid . . . . .	3
hybrid_plot . . . . .	5
set_layout . . . . .	6
<b>Index</b>	<b>7</b>

---

seqcombo-package      *seqcombo: Visualization Tool for Genetic Reassortment*

---

### Description

Provides useful functions for visualizing virus reassortment events.

### Author(s)

**Maintainer:** Guangchuang Yu <guangchuangyu@gmail.com>

### See Also

Useful links:

- Report bugs at <https://github.com/GuangchuangYu/seqcombo/issues>

---

geom\_genotype      *geom\_genotype*

---

### Description

geom layer of genotype

### Usage

```
geom_genotype(
  virus_info,
  v_color = "darkgreen",
  v_fill = "steelblue",
  v_shape = "ellipse",
  l_color = "black",
  asp = 1,
  g_height = 0.65,
  g_width = 0.65
)
```

### Arguments

virus_info	virus information
v_color	the color of outer boundary of virus; can use expression (e.g. v_color=~Host) to color virus by specific variable
v_fill	the color to fill viruses; can use expression (e.g. v_fill=~Host) to fill virus by specific variable
v_shape	one of 'hexagon' or 'ellipse'

l_color	color of the lines that indicate genetic flow
asp	aspect ratio of the plotting device
g_height	height of regions to plot gene segments relative to the virus
g_width	width of gene segment relative to width of the virus (the hexagon)

**Value**

geom layer

**Author(s)**

Guangchuang Yu

**Examples**

```
library(tibble)
library(ggplot2)
n <- 8
virus_info <- tibble(id = 1:7,
  x = c(rep(1990, 4), rep(2000, 2), 2009),
  y = c(1,2,3,5, 1.5, 3, 4),
  segment_color = list(rep('purple', n),
    rep('red', n), rep('darkgreen', n), rep('lightgreen', n),
    c('darkgreen', 'darkgreen', 'red', 'darkgreen', 'red', 'purple', 'red', 'purple'),
    c('darkgreen', 'darkgreen', 'red', 'darkgreen', 'darkgreen', 'purple', 'red', 'purple'),
    c('darkgreen', 'lightgreen', 'lightgreen', 'darkgreen', 'darkgreen', 'purple', 'red', 'purple'))))
ggplot() + geom_genotype(virus_info)
```

---

geom\_hybrid

*geom\_hybrid*

---

**Description**

geom layer for reassortment events

**Usage**

```
geom_hybrid(
  virus_info,
  flow_info,
  v_color = "darkgreen",
  v_fill = "steelblue",
  v_shape = "ellipse",
  l_color = "black",
  asp = 1,
  parse = FALSE,
  g_height = 0.65,
  g_width = 0.65,
```

```

    t_size = 3.88,
    t_color = "black"
  )

```

### Arguments

virus_info	virus information
flow_info	flow information
v_color	the color of outer boundary of virus; can use expression (e.g. v_color=~Host) to color virus by specific variable
v_fill	the color to fill viruses; can use expression (e.g. v_fill=~Host) to fill virus by specific variable
v_shape	one of 'hexagon' or 'ellipse'
l_color	color of the lines that indicate genetic flow
asp	aspect ratio of the plotting device
parse	whether parse label, only works if 'label' and 'label_position' exist
g_height	height of regions to plot gene segments relative to the virus
g_width	width of gene segment relative to width of the virus (the hexagon)
t_size	size of text label
t_color	color of text label

### Value

geom layer

### Author(s)

Guangchuang Yu

### Examples

```

library(tibble)
library(ggplot2)
n <- 8
virus_info <- tibble(id = 1:7,
  x = c(rep(1990, 4), rep(2000, 2), 2009),
  y = c(1,2,3,5, 1.5, 3, 4),
  segment_color = list(rep('purple', n),
    rep('red', n), rep('darkgreen', n), rep('lightgreen', n),
    c('darkgreen', 'darkgreen', 'red', 'darkgreen', 'red', 'purple', 'red', 'purple'),
    c('darkgreen', 'darkgreen', 'red', 'darkgreen', 'darkgreen', 'purple', 'red', 'purple'),
    c('darkgreen', 'lightgreen', 'lightgreen', 'darkgreen', 'darkgreen', 'purple', 'red', 'purple')))

flow_info <- tibble(from = c(1,2,3,3,4,5,6), to = c(5,5,5,6,7,6,7))

ggplot() + geom_hybrid(virus_info, flow_info)

```

---

hybrid_plot	<i>hyrid_plot</i>
-------------	-------------------

---

**Description**

visualize virus reassortment events

**Usage**

```
hybrid_plot(
  virus_info,
  flow_info,
  v_color = "darkgreen",
  v_fill = "steelblue",
  v_shape = "ellipse",
  l_color = "black",
  asp = 1,
  parse = FALSE,
  g_height = 0.65,
  g_width = 0.65,
  t_size = 3.88,
  t_color = "black"
)
```

**Arguments**

virus_info	virus information
flow_info	flow information
v_color	the color of outer boundary of virus; can use expression (e.g. v_color=~Host) to color virus by specific variable
v_fill	the color to fill viruses; can use expression (e.g. v_fill=~Host) to fill virus by specific variable
v_shape	one of 'hexagon' or 'ellipse'
l_color	color of the lines that indicate genetic flow
asp	aspect ratio of the plotting device
parse	whether parse label, only works if 'label' and 'label_position' exist
g_height	height of regions to plot gene segments relative to the virus
g_width	width of gene segment relative to width of the virus (the hexagon)
t_size	size of text label
t_color	color of text label

**Value**

ggplot object

**Author(s)**

Guangchuang Yu

**Examples**

```
library(tibble)
n <- 8
virus_info <- tibble(id = 1:7,
  x = c(rep(1990, 4), rep(2000, 2), 2009),
  y = c(1,2,3,5, 1.5, 3, 4),
  segment_color = list(rep('purple', n),
    rep('red', n), rep('darkgreen', n), rep('lightgreen', n),
    c('darkgreen', 'darkgreen', 'red', 'darkgreen', 'red', 'purple', 'red', 'purple'),
    c('darkgreen', 'darkgreen', 'red', 'darkgreen', 'darkgreen', 'purple', 'red', 'purple'),
    c('darkgreen', 'lightgreen', 'lightgreen', 'darkgreen', 'darkgreen', 'purple', 'red', 'purple')))

flow_info <- tibble(from = c(1,2,3,3,4,5,6), to = c(5,5,5,6,7,6,7))

hybrid_plot(virus_info, flow_info)
```

---

`set_layout`*set\_layout*

---

**Description**

set layout for reassortment plot

**Usage**`set_layout(virus_info, flow_info, layout = "layout.auto")`**Arguments**

<code>virus_info</code>	virus information
<code>flow_info</code>	flow information
<code>layout</code>	layout method

**Value**

updated virus\_info

**Author(s)**

Guangchuang Yu

# Index

\* **internal**

seqcombo-package, [2](#)

geom\_genotype, [2](#)

geom\_hybrid, [3](#)

hybrid\_plot, [5](#)

seqcombo (seqcombo-package), [2](#)

seqcombo-package, [2](#)

set\_layout, [6](#)